

sequencelisting-21407.ST25  
SEQUENCE LISTING

&lt;110&gt; Roche Vitamins AG

&lt;120&gt; SQS gene

&lt;130&gt; NDR5218

&lt;160&gt; 8

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 4807

&lt;212&gt; DNA

&lt;213&gt; Phaffia rhodozyma

&lt;220&gt;

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&lt;222&gt; (1550)..(1577)

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&lt;222&gt; (4106)..(4107)

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&lt;222&gt; (1469)..(1470)

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sequencelisting-21407.ST25

&lt;222&gt; (3959)..(3970)

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&lt;221&gt; Intron

&lt;222&gt; (3882)..(3958)

&lt;223&gt;

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (3567)..(3881)

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&lt;222&gt; (1755)..(1766)

&lt;223&gt;

&lt;220&gt;

&lt;221&gt; Intron

&lt;222&gt; (1578)..(1752)

&lt;223&gt;

&lt;400&gt; 1

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Ser Asp Tyr Leu Val Leu						
5						
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		Val His Ala Ser				
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tatgatcgct	tgtgctaccg	tctttcttgg	aaatccttcc	catcag gc	cga tct Cys Arg Ser 15	1890
gcg agc ttt aat gca gta cgc gat ctg gca tga gcc tcg aag gaa tat						1938
Ala Ser Phe Asn Ala Val Arg Asp Leu Ala						
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cac tgc aca gga gga aca tgc aac atc cgg ttg gga ccg aga aac tat						1986
His Cys Thr Gly Gly Thr Cys Asn Ile Arg Leu Gly Pro Arg Asn Tyr						
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gaa gga atg ttg gaa gta ttt gga tct gac ttc aag aag ttt cgc agc						2034
Glu Gly Met Leu Glu Val Phe Gly Ser Asp Phe Lys Lys Phe Arg Ser						
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Cys His Gln Arg Val Gly Arg Arg Ser Tyr Pro Ser						
	65		70		75	
tcattcttctc	tctcctttga	gatctggtcg	cctccgcatt	ttcttggtgc	agaagggtca	2141
gaagctgaca	acaccatctc	tactgttcgg	gacacggcta	g at	ctg ttt att cta His Leu Phe Ile Leu 80	2196
tct cgc tct tcg agg act gga tac cat tga gga tga cat gag tct atc						2244
Ser Arg Ser Ser Arg Thr Gly Tyr His						
	85		90			
taa tga tgt gaa gct tcc cct gct tcg gac att ctg gga aaa gct tga						2292
	Cys Glu Ala Ser Pro Ala Ser Asp Ile Leu Gly Lys Ala					
	95		100		105	
ctc ccc tgg gtg gac ctt tac tgg atc cgg tcc aaa tga gaa gga tag						2340
Leu Pro Trp Val Asp Leu Tyr Trp Ile Arg Ser Lys						
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aga gct tct tgt tca ctt cga tgt ggc cat cgc cga gtt tgc caa ctt						2388
Arg Ala Ser Cys Ser Leu Arg Cys Gly His Arg Arg Val Cys Gln Leu						
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Gly Arg						
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gcc ctc caa gcc tgt ggc cga ggt cca gtc gac cga aga ttt caa cct	2594
Ala Leu Gln Ala Cys Gly Arg Gly Pro Val Asp Arg Arg Phe Gln Pro	
165 170 175	
ata ctg tca tta cgt cgc tgg act cgt cgg cga ggg act ctc ccg act	2642
Ile Leu Ser Leu Arg Arg Trp Thr Arg Arg Arg Gly Thr Leu Pro Thr	
180 185 190	
ctt tgt cgc gac cga gaa gga acg acc att ctt ggc caa cca gat ggt	2690
Leu Cys Arg Asp Arg Glu Gly Thr Thr Ile Leu Gly Gln Pro Asp Gly	
195 200 205 210	
act ttc aaa ctc gtt cgg act cct tct cca aaa gac aaa cat cct tcg	2738
Thr Phe Lys Leu Val Arg Thr Pro Ser Pro Lys Asp Lys His Pro Ser	
215 220 225	
aga tat tcg gga gga cgc cga cga agg tcg tgg ctt ctg gcc aag aga	2786
Arg Tyr Ser Gly Gly Arg Arg Arg Arg Ser Trp Leu Leu Ala Lys Arg	
230 235 240	
gat ctg ggc caa ccc gat cta tac tgc gca tgc acc ggg cac aag gtt	2834
Asp Leu Gly Gln Pro Asp Leu Tyr Cys Ala Cys Thr Gly His Lys Val	
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taa ctc gtt gac tga cct ggt caa gaa aga aaa cat cga caa agg atc	2882
Leu Val Asp Pro Gly Gln Glu Arg Lys His Arg Gln Arg Ile	
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Asn Val Gly Val Glu Cys Asp Asp Thr Arg Arg Asp His Pro Tyr Tyr	
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Arg Arg Thr Gly Leu Pro Leu Thr Ser Lys Glu Pro Glu Cys Phe Gln	
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ctt ttg tgc tat ccc ggc tgt cat gtc gat tgc aac gtt gga gct atg	3026
Leu Leu Cys Tyr Pro Gly Cys His Val Asp Cys Asn Val Gly Ala Met	
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Leu His Glu Pro Ser Gly Val Pro Thr Lys His Lys Asn Gln Lys Gly	
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Arg Ser Arg Arg	
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Val Gln Gln Pro Ser Gly Gly Gly Ile His Val Arg Leu Cys Ser	
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Lys Asp Ser Cys Gln Gly Tyr Ser Tyr Arg Ser Leu His Gln Val	
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 375 380

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 Asn Arg Thr Met Gly Ala  
 385

cttcaagttt cctctcgctt catctttgtt gagaagaggg atctgatgta tctttctttg 3554  
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 Leu Pro Leu Ile Tyr Asp Asp Ser Ala Phe Glu Pro  
 390 395

tca aaa ccc cgc acc ctc aac ggc gct tga ccc ttt ctc agg aga cgc 3652  
 Ser Lys Pro Arg Thr Leu Asn Gly Ala Pro Phe Leu Arg Arg Arg  
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tcg ttt aag gat agc ctc taa gaa ggc tga gat cac cgc cgc tgc tct 3700  
 Ser Phe Lys Asp Ser Leu Glu Gly Asp His Arg Arg Cys Ser  
 415 420 425

tgt cag gaa gaa agc ccg gga tca cgc taa gtg gag aga gtc caa ggg 3748  
 Cys Gln Glu Glu Ser Pro Gly Ser Arg Val Glu Arg Val Gln Gly  
 430 435 440

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 Ile Ala Ser Glu Arg Ser Glu Gln Ala Gly Gln Leu Gly Gly Cys  
 445 450 455

ttg ggt att gat cgg cgg tat gat cgt tgg att gtt gct cgt gat ggg 3844  
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 Val Ala Ile

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&lt;210&gt; 2

&lt;211&gt; 1536

&lt;212&gt; DNA

<213> *Phaffia rhodozyma*

&lt;220&gt;

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&lt;222&gt; (1)..(1536)

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Leu Arg Ala Leu Met Gln Tyr Ala Ile Trp His Glu Pro Arg Arg Asn	
20 25 30	
atc act gca cag gag gaa cat gca aca tcc ggt tgg gac cga gaa act	144
Ile Thr Ala Gln Glu Glu His Ala Thr Ser Gly Trp Asp Arg Glu Thr	
35 40 45	
atg aag gaa tgt tgg aag tat ttg gat ctg act tca aga agt ttc gca	192
Met Lys Glu Cys Trp Lys Tyr Leu Asp Leu Thr Ser Arg Ser Phe Ala	
50 55 60	
gct gtc atc aaa gag ttg gac gga gat ctt acc cga gtc atc tgt tta	240
Ala Val Ile Lys Glu Leu Asp Gly Asp Leu Thr Arg Val Ile Cys Leu	
65 70 75 80	
ttc tat ctc gct ctt cga gga ctg gat acc att gag gat gac atg agt	288
Phe Tyr Leu Ala Leu Arg Gly Leu Asp Thr Ile Glu Asp Asp Met Ser	
85 90 95	
cta tct aat gat gtg aag ctt ccc ctg ctt cgg aca ttc tgg gaa aag	336
Leu Ser Asn Asp Val Lys Leu Pro Leu Leu Arg Thr Phe Trp Glu Lys	
100 105 110	
ctt gac tcc cct ggg tgg acc ttt act gga tcc ggt cca aat gag aag	384
Leu Asp Ser Pro Gly Trp Thr Phe Thr Gly Ser Gly Pro Asn Glu Lys	
115 120 125	
gat aga gag ctt ctt gtt cac ttc gat gtg gcc atc gcc gag ttt gcc	432
Asp Arg Glu Leu Leu Val His Phe Asp Val Ala Ile Ala Glu Phe Ala	
130 135 140	
aac ttg gac gtc aac tct cgg aac gtc att cga gac atc act cgc aag	480
Asn Leu Asp Val Asn Ser Arg Asn Val Ile Arg Asp Ile Thr Arg Lys	
145 150 155 160	



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Pro Val Ala Glu Val Gln Ser Thr Glu Asp Phe Asn Leu Tyr Cys His	
180 185 190	
tac gtc gct gga ctc gtc ggc gag gga ctc tcc cga ctc ttt gtc gcg	624
Tyr Val Ala Gly Leu Val Gly Glu Gly Leu Ser Arg Leu Phe Val Ala	
195 200 205	
acc gag aag gaa cga cca ttc ttg gcc aac cag atg gta ctt tca aac	672
Thr Glu Lys Glu Arg Pro Phe Leu Ala Asn Gln Met Val Leu Ser Asn	
210 215 220	
tcg ttc gga ctc ctt ctc caa aag aca aac atc ctt cga gat att cgg	720
Ser Phe Gly Leu Leu Leu Gln Lys Thr Asn Ile Leu Arg Asp Ile Arg	
225 230 235 240	
gag gac gcc gac gaa ggt cgt ggc ttc tgg cca aga gag atc tgg gcc	768
Glu Asp Ala Asp Glu Gly Arg Gly Phe Trp Pro Arg Glu Ile Trp Ala	
245 250 255	
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260 265 270	
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275 280 285	
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Leu Ser Ala Met Thr Leu Asp Ala Ile Thr His Thr Thr Asp Ala Leu	
290 295 300	
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Asp Tyr Leu Ser Leu Leu Lys Asn Gln Ser Val Phe Asn Phe Cys Ala	
305 310 315 320	
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Ile Pro Ala Val Met Ser Ile Ala Thr Leu Glu Leu Cys Phe Met Asn	
325 330 335	
cca gcg gtg ttc caa cga aac ata aaa atc aga aag gga gaa gcc gtc	1056
Pro Ala Val Phe Gln Arg Asn Ile Lys Ile Arg Lys Gly Glu Ala Val	
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gag ctc att atg aag tgc aac aac cct cgg gag gtg gca tac atg ttt	1104
Glu Leu Ile Met Lys Cys Asn Asn Pro Arg Glu Val Ala Tyr Met Phe	
355 360 365	
aga gat tat gct cga aag att cat gcc aag gct att cct aca gat cct	1152
Arg Asp Tyr Ala Arg Lys Ile His Ala Lys Ala Ile Pro Thr Asp Pro	
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Asn Phe Ile Lys Leu Ser Val Ala Cys Gly Arg Ile Glu Gln Trp Ala	
385 390 395 400	
gag cac tac tac ccc tca ttt atg atg att cgg cct tcg aat gac cct	1248
Glu His Tyr Tyr Pro Ser Phe Met Met Ile Arg Pro Ser Asn Asp Pro	
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caa aac ccc gca ccc tca acg gcg ctt gac cct ttc tca gga gac gct	1296
Gln Asn Pro Ala Pro Ser Thr Ala Leu Asp Pro Phe Ser Gly Asp Ala	
420 425 430	

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Val Arg Lys Lys Ala Arg Asp His Ala Lys Trp Arg Glu Ser Lys Gly
      450      455      460

ttg cct ccg agc gat ccg aac aag ccg gac aac tcg gag gat gtt aat      1440
Leu Pro Pro Ser Asp Pro Asn Lys Pro Asp Asn Ser Glu Asp Val Asn
      465      470      475      480

tgg gta ttg atc ggc ggt atg atc gtt gga ttg ttg ctc gtg atg ggc      1488
Trp Val Leu Ile Gly Gly Met Ile Val Gly Leu Leu Leu Val Met Gly
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gtg ctc ggt ttg gct atc gct tgg gtt gtt ctt cag ttt gag caa taa      1536
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&lt;211&gt; 511

&lt;212&gt; PRT

&lt;213&gt; Phaffia rhodozyma

&lt;400&gt; . 3

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      20      25      30

Ile Thr Ala Gln Glu Glu His Ala Thr Ser Gly Trp Asp Arg Glu Thr
      35      40      45

Met Lys Glu Cys Trp Lys Tyr Leu Asp Leu Thr Ser Arg Ser Phe Ala
50      55      60

Ala Val Ile Lys Glu Leu Asp Gly Asp Leu Thr Arg Val Ile Cys Leu
65      70      75      80

Phe Tyr Leu Ala Leu Arg Gly Leu Asp Thr Ile Glu Asp Asp Met Ser
      85      90      95

Leu Ser Asn Asp Val Lys Leu Pro Leu Leu Arg Thr Phe Trp Glu Lys
      100      105      110

Leu Asp Ser Pro Gly Trp Thr Phe Thr Gly Ser Gly Pro Asn Glu Lys
      115      120      125

Asp Arg Glu Leu Leu Val His Phe Asp Val Ala Ile Ala Glu Phe Ala
130      135      140

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 Met Gly Asn Gly Met Ala Asp Phe Ala Ser Leu Ser Thr Pro Ser Lys  
 165 170 175  
 Pro Val Ala Glu Val Gln Ser Thr Glu Asp Phe Asn Leu Tyr Cys His  
 180 185 190  
 Tyr Val Ala Gly Leu Val Gly Glu Gly Leu Ser Arg Leu Phe Val Ala  
 195 200 205  
 Thr Glu Lys Glu Arg Pro Phe Leu Ala Asn Gln Met Val Leu Ser Asn  
 210 215 220  
 Ser Phe Gly Leu Leu Leu Gln Lys Thr Asn Ile Leu Arg Asp Ile Arg  
 225 230 235 240  
 Glu Asp Ala Asp Glu Gly Arg Gly Phe Trp Pro Arg Glu Ile Trp Ala  
 245 250 255  
 Asn Pro Ile Tyr Thr Ala His Ala Pro Gly Thr Arg Phe Asn Ser Leu  
 260 265 270  
 Thr Asp Leu Val Lys Lys Glu Asn Ile Asp Lys Gly Ser Met Trp Val  
 275 280 285  
 Leu Ser Ala Met Thr Leu Asp Ala Ile Thr His Thr Thr Asp Ala Leu  
 290 295 300  
 Asp Tyr Leu Ser Leu Leu Lys Asn Gln Ser Val Phe Asn Phe Cys Ala  
 305 310 315 320  
 Ile Pro Ala Val Met Ser Ile Ala Thr Leu Glu Leu Cys Phe Met Asn  
 325 330 335  
 Pro Ala Val Phe Gln Arg Asn Ile Lys Ile Arg Lys Gly Glu Ala Val  
 340 345 350  
 Glu Leu Ile Met Lys Cys Asn Asn Pro Arg Glu Val Ala Tyr Met Phe  
 355 360 365  
 Arg Asp Tyr Ala Arg Lys Ile His Ala Lys Ala Ile Pro Thr Asp Pro  
 370 375 380  
 Asn Phe Ile Lys Leu Ser Val Ala Cys Gly Arg Ile Glu Gln Trp Ala  
 385 390 395 400  
 Glu His Tyr Tyr Pro Ser Phe Met Met Ile Arg Pro Ser Asn Asp Pro  
 405 410 415

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Gln Asn Pro Ala Pro Ser Thr Ala Leu Asp Pro Phe Ser Gly Asp Ala  
                   420                  425                  430

Arg Leu Arg Ile Ala Ser Lys Lys Ala Glu Ile Thr Ala Ala Ala Leu  
           435                  440                  445

Val Arg Lys Lys Ala Arg Asp His Ala Lys Trp Arg Glu Ser Lys Gly  
       450                  455                  460

Leu Pro Pro Ser Asp Pro Asn Lys Pro Asp Asn Ser Glu Asp Val Asn  
   465                  470                  475                  480

Trp Val Leu Ile Gly Gly Met Ile Val Gly Leu Leu Leu Val Met Gly  
                   485                  490                  495

Val Leu Gly Leu Ala Ile Ala Trp Val Val Leu Gln Phe Glu Gln  
           500                  505                  510

<210> 4

<211> 27

<212> DNA

<213> Artificial

<220>

<221> misc\_feature

<222> (3)..(3)

<223> n = a, c, g or t

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<222> (4)..(4)

<223> y = c or t

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<222> (6)..(6)

<223> n = a, c, g or t

<220>

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&lt;222&gt; (12)..(12)

&lt;223&gt; n = a, c, g or t

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (15)..(15)

&lt;223&gt; n = a, c, g or t

&lt;400&gt; 4

gcnytngaya cngtngarga ygayatg

27

&lt;210&gt; 5

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial

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&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (9)..(9)

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&lt;220&gt;

&lt;221&gt; misc\_feature

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&lt;222&gt; (18)..(18)

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26

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&lt;210&gt; 7

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&lt;400&gt; 7

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20

&lt;210&gt; 8

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;400&gt; 8

ccagatctct cttggccaga

20